High-throughput epitope identification for snakebite antivenom

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High-throughput epitope identification for snakebite antivenom

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Introduction
Insight into the epitopic recognition pattern for polyclonal antivenoms is a strong tool for accurate prediction of antivenom cross-reactivity and provides a basis for design of novel antivenoms. In this work, a high-throughput approach was applied to characterize linear epitopes in 966 individual toxins from pit vipers (Crotalidae) using the ICP Crotalidae antivenom. Due to an abundance of snake venom metalloproteinases and phospholipase A2 in the venomous species used for production of the investigated antivenom, this study focuses on these toxin families.

Objectives
- Identify epitopes in toxins used in immunization
- Characterize tolerated amino acid substitutions in identified epitopes
- Predict cross-reactivity of antivenom

Epitopes locate to surface regions

To identify epitopes, observed peptide specific signal intensities were mapped back to the amino acid sequence of each pit viper toxin. Using two or more overlapping 15-mer peptides with median signals above 20 AU, epitope core sequences were localized and subsequently mapped to crystal structures or homology models. As examples, P4 metalloproteinase and lyso49-phospholipase A2 from Bothrops asper (venom used in antivenom production) are presented here.

Conclusions
- Custom-designed high density peptide microarray technology enables parallel automated identification of epitopes in hundreds of toxins.
- Integrating multiple sequence alignment allows investigation of the effect of epitope variation on antivenom recognition.
- Cross-reactivity of antivenom is correlated to the degree of conservation in toxin epitopes and flanking residues.

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References

The α-helical region is highlighted in blue except for the high-signal epitope in Bothrops asper P4 metalloproteinase that is highlighted in red. All epitopes are found to be exposed on the protein surface. The structure of the metalloproteinase (PDB: 2W13) was obtained from the Protein Data Bank (pdb.org), and the homology model of the phospholipase A2 was built using CPHmodels1 based on a crystal structure of the lyso49-phospholipase from B. moojeni (PDB: 4KF1) with 87.7% identity.